

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga
Hawkins, Phillip R.
Hillman, Jennifer L.
Lal, Preeti
Goli, Surya K.

(ii) TITLE OF THE INVENTION: NOVEL HUMAN SERINE CARBOXYPEPTIDASE

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0241 US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: MPHGN0T03
(B) CLONE: 443004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15
 Pro Gly Pro Cys Asp Gly Leu Phe His Ser Leu Tyr Arg Ser Val Ser
 20 25 30
 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45
 Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60
 Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Asp Phe Leu Thr Val
 65 70 75 80
 Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
 85 90 95
 Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Glu Pro
 100 105 110
 Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
 115 120 125
 Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
 130 135 140
 Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
 145 150 155 160
 Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
 165 170 175
 Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
 180 185 190
 Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
 195 200 205
 Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
 210 215 220
 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
 225 230 235 240
 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
 245 250 255
 Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
 260 265 270
 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
 275 280 285
 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
 290 295 300
 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
 305 310 315 320
 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
 325 330 335
 Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
 340 345 350
 Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365
 Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380
 Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400
 Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415
 Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Gly Val Ala Gly Tyr
 420 425 430
 Ile Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly
 435 440 445
 His Thr Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn

450	455	460										
Arg	Phe	Ile	Tyr	Gly	Lys	Gly	Trp	Asp	Pro	Tyr	Val	Gly
465												
					470							475

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MPHGN0T03
- (B) CLONE: 443004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGCGCTGCA	AGGACAAACCG	GCTGGGGTCC	TTGCGCGCCG	GGCTCAGGGA	GGAGCACCAGA	60
CTGCGCCGCA	CCCTGAGAGA	TGGTTGGTGC	CATGTGGAAG	GTGATTGTTT	CGCTGGTCCT	120
GTTGATGCCT	GGCCCTGTG	ATGGGCTGTT	TCACTCCCTA	TACAGAAGTG	TTTCCATGCC	180
ACCTAAAGGA	GACTCAGGAC	AGCCATTATT	TCTCACCCCT	TACATTGAAG	CTGGGAAGAT	240
CCAAAAAGGA	AGAGAAATTGA	GTTTGGTCGG	TCCTTTCCA	GGACTGAACA	TGAAGAGTTA	300
TGCCGACTTC	CTCACTGTGA	ATAAGACTTA	CAACAGCAAC	CTCTTCTTCT	GGTTCTTCCC	360
AGCTCAGATA	CAGCCAGAAG	ATGCCCCAGT	AGTTCTCTGG	CTACAGGGTG	AGCCGGGAGG	420
TTCATCCATG	TTGGACTCT	TTGTGGAACA	TGGGCCTTAT	GTTGTCACAA	GTAACATGAC	480
CTTGCCTGAC	AGAGACTTCC	CCTGGACCAC	AACGCTCTCC	ATGCCTTACA	TTGACAATCC	540
AGTGGGCACA	GGCTTCAGTT	TTACTGATGA	TACCCACGGA	TATGCACTCA	ATGAGGACGA	600
TGTAGCACGG	GATTTATACA	GTGCACTAAT	TCAGTTTTTC	CAGATATTTC	CTGAATATAA	660
AAATAATGAC	TTTTATGTCA	CTGGGGAGTC	TTATGAGGG	AAATATGTGC	CAGCCATTGC	720
ACACCTCATC	CATTCCCTCA	ACCCCTGTGAG	AGAGGTGAAG	ATCAACCTGA	ACGGAATTGC	780
TATTGGAGAT	GGATATTCTG	ATCCCAGATC	AATTATAGGG	GGCTATGCAG	AATTCTGTGA	840
CCAAATTGGC	TTGTTGGATG	AGAAGCAAA	AAAGTACTTC	CAGAAGCAGT	GCCATGAATG	900
CATAGAACAC	ATCAGGAAGC	AGAACTGGTT	TGAGGCCCTT	GAAATACTGG	ATAAACTACT	960
AGATGGCGAC	TTAACAAAGT	ATCCTTCTTA	CTTCCAGAAT	GTTACAGGAT	GTAGTAATTA	1020
CTATAACTTT	TTGCGGTGCA	CGGAACCTGA	GGATCAGCTT	TACTATGTGA	AATTCTGTCA	1080
ACTCCCAGAG	GTGAGACAAG	CCATCCACGT	GGGGATCAG	ACTTTAATG	ATGGAACTAT	1140
AGTTGAAAG	TACTTGCAG	AAGATACAGT	ACAGTCAGTT	AAGCCATGGT	TAACTGAAAT	1200
CATGAATAAT	TATAAGGTT	TGATCTACAA	TGGCCAACCTG	GACATCATCG	TGGCAGCTGC	1260
CCTGACAGAG	CGCTCCTTGA	TGGCATGGA	CTGGAAAGGA	TCCCAGGAAT	ACAAGAAGGC	1320
AGAAAAAAA	AAAGTTTGA	AGATCTTAA	ATCTGACAGT	GGAGTGGCTG	GTTACATCCG	1380
GCAAGTGGGT	GACTTCCATC	AGGTAAATTAT	TCGAGGGGGA	GGACATACTT	TACCCATGAA	1440
CCAGCCTCTG	AGAGCTTTG	ACATGATTAA	TCGATTCTATT	TATGGAAAAG	GATGGGATCC	1500
TTATGTTGGA	TAAACTACCT	TCCCCAAAAGA	GAACATCAGA	GGTTTTCATT	GCTGAAAAGA	1560
AAATCGTAA	AACAGAAAAT	GTCATAGGAA	TAAAAAAATT	ATCTTTTCAT	ATCTGCAAGA	1620
TCTTTTCAT	CAATAAAAAT	TATCCTTGAA	ACAAAAAAA	AAAGAAAAAG		1670

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT01
- (B) CLONE: 566993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15
 Pro Gly Pro Cys Asp Gly Leu Phe His Ser Leu Tyr Arg Ser Val Ser
 20 25 30
 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45
 Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60
 Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
 65 70 75 80
 Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
 85 90 95
 Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
 100 105 110
 Gly Gly Ser Ser Met Xaa Gly Leu Phe Val Glu His Gly Pro Tyr Val
 115 120 125
 Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
 130 135 140
 Thr Xaa Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
 145 150 155 160
 Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
 165 170 175
 Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
 180 185 190
 Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
 195 200 205
 Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
 210 215 220
 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
 225 230 235 240
 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
 245 250 255
 Gly Leu Leu Asp Glu Lys Gln Lys Tyr Phe Gln Lys Gln Cys His
 260 265 270
 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
 275 280 285
 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
 290 295 300
 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
 305 310 315 320
 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
 325 330 335
 Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
 340 345 350
 Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365
 Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380
 Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400
 Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415
 Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430
 Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His
 435 440 445
 Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg

450	455	460
Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly		
465	470	475

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT01
- (B) CLONE: 566993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAAAGCTGGT	ACGCCTGCNG	GTNCGGTCC	GGAATTNCNG	GGTNGACCCA	CGCGTCCGAN	60
CGACTGCGCC	GCACCCCTGAG	AGATGGTTGG	TGCCATGTGG	AAGGTGATTG	TTTCGCTGGT	120
CCTGTTGATG	CCTGGCCCT	GTGATGGGCT	GTTCACATCC	CTATACAGAA	GTGTTTCCAT	180
GCCACCTAAG	GGAGACTCAG	GACAGCCATT	ATTTCTCACC	CCTTACATTG	AAGCTGGAA	240
GATCCAAAAA	GGAAGAGAAAT	TGAGTTTGGT	CGGCCCTTC	CCAGGACTGA	ACATGAAGAG	300
TTATGCCGGC	TTCCTCACCG	TGAATAAGAC	TTACAACAGC	AACCTCTCT	TCTGGTTCTT	360
CCCAGCTCAG	ATACAGCCAG	AAGATGCCCC	AGTAGTTCTC	TGGCTACAGG	GTGGGCCGGG	420
AGGTTCATCC	ATGTTWGGAC	TCTTGTTGGA	ACATGGGCCT	TATGTTGTCA	CAAGTAACAT	480
GACCTTGCCT	GACAGAGACT	TCCCCTGGAC	CACAACGSTC	TCCATGCTTT	ACATTGACAA	540
TCCAGTGGGC	ACAGGCTTCA	GTTTTACTGA	TGATACCCAC	GGATATGCAG	TCAATGAGGA	600
CGATGTAGCA	CGGGATTAT	ACAGTGCACT	AATTCAAGTT	TTCCAGATAT	TTCCTGAATA	660
TAAAAATAAT	GACTTTTATG	TCACTGGGA	GTCTTATGCA	GGGAAATATG	TGCCAGCCAT	720
TGCACACCTC	ATCCATTCCC	TCAACCCGT	GAGAGAGGTG	AAGATCAACC	TGAACGGAAT	780
TGCTATTGGA	GATGGATATT	CTGATCCCGA	ATCAATTATA	GGGGGCTATG	CAGAATTCCCT	840
GTACCAAATT	GGCTTGTGG	ATGAGAAGCA	AAAAAAAGTAC	TTCCAGAAGC	AGTGCCATGA	900
ATGCATAGAA	CACATCAGGA	AGCAGAACTG	GTGTTGAGGCC	TTTGAAATAC	TGGATAAACT	960
ACTAGATGGC	GACTTAACAA	GTGATCCTTC	TTACTTCCAG	AATGTTACAG	GATGTAGTAA	1020
TTACTATAAC	TTTTGCGGT	GCACCGAAC	TGAGGATCAG	CTTTACTATG	TGAAATTTTT	1080
GTCACTCCCA	GAGGTGAGAC	AAGCCATCCA	CGTGGGAAT	CAGACTTTA	ATGATGGAAC	1140
TATAGTTGAA	AAGTACTTGC	GAGAAGATAC	AGTACAGTCA	GTAAAGCCAT	GGTTAACTGA	1200
AATCATGAAT	AATTATAAGG	TTCTGATCTA	CAATGGCCTA	CTGGACATCA	TCGTGGCAGC	1260
TGCCCTGACA	GAGCGCTCCT	TGATGGGCAT	GGACTGGAAA	GGTTCCCAGG	AATACAAGAA	1320
GGCAGAAAAA	AAAGTTGGA	AGATCTTAA	ATCTGACAGT	GAAGTGGCTG	GTTACATCCG	1380
GCAAGTGGGT	GACTTCCATC	AGGTAATTAT	TCGAGGTGGA	GGACATATTT	TACCCTATGA	1440
CCAGCCTCTG	AGAGCTTTG	ACATGATTAA	TCGATTCTT	TATGGAAAAG	GATGGGATCC	1500
TTATGTTGGA	TAAACTACCT	TCCCCAAAGA	GAACATCAGA	GGTTTCATN	T	1551

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCRT01
- (B) CLONE: 770469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15
 Pro Gly Pro Cys Gly Gly Leu Phe His Ser Leu Tyr Arg Ser Val Ser
 20 25 30
 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45
 Ile Glu Ala Gly Lys Ile Tyr Thr Gly Thr Asn Ser Val Phe Gln Ile
 50 55 60
 Phe Pro Glu Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr
 65 70 75 80
 Ala Gly Lys Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn
 85 90 95
 Pro Val Arg Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp
 100 105 110
 Gly Tyr Ser Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu
 115 120 125
 Tyr Gln Ile Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys
 130 135 140
 Gln Cys His Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu
 145 150 155 160
 Ala Phe Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp
 165 170 175
 Pro Ser Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe
 180 185 190
 Leu Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu
 195 200 205
 Ser Leu Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe
 210 215 220
 Asn Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln
 225 230 235 240
 Ser Val Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu
 245 250 255
 Ile Tyr Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Leu Thr Glu
 260 265 270
 Arg Ser Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys
 275 280 285
 Ala Glu Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala
 290 295 300
 Gly Tyr Ile Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly
 305 310 315 320
 Gly Gly His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met
 325 330 335
 Ile Asn Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 340 345 350

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCRT01
- (B) CLONE: 770469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGGCAAACC	GGCTGGGGTC	CTTGCGCGCC	GCGGCTCAGG	GAGGAGCACC	GAUTGCCCG	60
CACCCCTGAGA	GATGGTTGGT	GCCATGTGGA	AGGTGATTGT	TTCGCTGGTC	CTGTTGATGC	120
CTGGCCCCCTG	TGGTGGGCTG	TTTCACTCCC	TATACAGAAG	TGTTTCCATG	CCACCTAAGG	180
GAGACTCAGG	ACAGCCATTA	TTTCTCACCC	CTTACATTGA	AGCTGGGAAG	ATTTATACAG	240
GCACTAATTG	AGTTTCCAG	ATATTCCTG	AATATAAAA	TAATGACTTT	TATGTCACTG	300
GGGAGTCTTA	TGCAGGGAAA	TATGTGCCAG	CCATTGCACA	CCTCATCCAT	TCCCTCAACC	360
CTGTGAGAGA	GGTGAAGATC	AACCTGAACG	GAATTGCTAT	TGGAGATGGA	TATTCTGATC	420
CCGAATCAAT	TATAGGGGGC	TATGCAGAAT	TCCTGTACCA	AATTGGCTTG	TTGGATGAGA	480
AGCAAAAAAA	GTACTTCCAG	AAGCAGTGCC	ATGAATGCAT	AGAACACATC	AGGAAGCAGA	540
ACTGGTTGAA	GGCCTTGAA	ATACTGGATA	AACTACTAGA	TGGCGACTTA	ACAAGTGATC	600
CTTCTTACTT	CCAGAATGTT	ACAGGATGTA	GTAATTACTA	TAACTTTTG	CGGTGCACGG	660
AACCTGAGGA	TCAGCTTAC	TATGTGAAAT	TTTTGTCACT	CCCAGAGGTG	AGACAAGCCA	720
TCCACGTGGG	GAATCAGACT	TTTAATGATG	GAACTATAGT	TGAAAAGTAC	TTGCGAGAAG	780
ATACAGTACA	GTCAGTTAAG	CCATGGTTAA	CTGAAATCAT	GAATAATTAT	AAGGTTCTGA	840
TCTACAATGG	CCAACGGAC	ATCATCGTGG	CAGCTGCCCT	GACAGAGCGC	TCCTTGATGG	900
GCATGGACTG	GAAAGGATCC	CAGGAATACA	AGAAGGCAGA	AAAAAAAGTT	TGGAAGATCT	960
TTAAATCTGA	CAGTGAAGTG	GCTGGTTACA	TCCGGCAAGT	GGGTGACTTC	CATCAGGTAA	1020
TTATTCGAGG	TGGAGGACAT	ATTTTACCCCT	ATGACCAGCC	TCTGAGAGCT	TTTGACATGA	1080
TTAACATCGATT	CATTTATGGA	AAAGGATGGG	ATCCTTATGT	TGGATAAAACT	ACCTTCCCAA	1140
AAGAGAACAT	CAGAGGTTTT	CATTGCTGAA	AAGAAAATCG	TAAAAAACAGA	AAATGTCATA	1200
GGAATAAAAAA	AATTATCTTT	TCATATCTGC	AAGATTTTTT	TCATCAATAA	AAATTATCCT	1260
					TGA	1263

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1718107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Val	Lys	Phe	His	Leu	Leu	Val	Leu	Ile	Ala	Phe	Thr	Cys	Tyr	Thr
1					5				10					15	
Cys	Ser	Asp	Ala	Thr	Leu	Trp	Asn	Pro	Tyr	Lys	Lys	Leu	Met	Arg	Gly
									20			25		30	
Ser	Ala	Ser	Pro	Pro	Arg	Pro	Gly	Glu	Ser	Gly	Glu	Pro	Leu	Phe	Leu
									35		40		45		
Thr	Pro	Leu	Leu	Gln	Asp	Gly	Lys	Ile	Glu	Glu	Ala	Arg	Asn	Lys	Ala
								50		55		60			
Arg	Val	Asn	His	Pro	Met	Leu	Ser	Ser	Val	Glu	Ser	Tyr	Ser	Gly	Phe
								65		70		75		80	
Met	Thr	Val	Asp	Ala	Lys	His	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Tyr	Val
								85		90		95			
Pro	Ala	Lys	Asn	Asn	Arg	Glu	Gln	Ala	Pro	Ile	Leu	Val	Trp	Leu	Gln
								100		105		110			
Gly	Gly	Pro	Gly	Ala	Ser	Ser	Leu	Phe	Gly	Met	Phe	Glu	Glu	Asn	Gly
								115		120		125			
Pro	Phe	His	Ile	His	Arg	Asn	Lys	Ser	Val	Lys	Gln	Arg	Glu	Tyr	Ser
								130		135		140			
Trp	His	Gln	Asn	His	His	Met	Ile	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr
								145		150		155		160	
Gly	Phe	Ser	Phe	Thr	Asp	Ser	Asp	Glu	Gly	Tyr	Ser	Thr	Asn	Glu	Glu
								165		170		175			

His Val Gly Glu Asn Leu Met Lys Phe Ile Gln Gln Phe Phe Val Leu
 180 185 190
 Phe Pro Asn Leu Leu Lys His Pro Phe Tyr Ile Ser Gly Glu Ser Tyr
 195 200 205
 Gly Gly Lys Phe Val Pro Ala Phe Gly Tyr Ala Ile His Asn Ser Gln
 210 215 220
 Ser Gln Pro Lys Ile Asn Leu Gln Gly Leu Ala Ile Gly Asp Gly Tyr
 225 230 235 240
 Thr Asp Pro Leu Asn Gln Leu Asn Tyr Gly Glu Tyr Leu Tyr Glu Leu
 245 250 255
 Gly Leu Ile Asp Leu Asn Gly Arg Lys Lys Phe Asp Glu Asp Thr Ala
 260 265 270
 Ala Ala Ile Ala Cys Ala Glu Arg Lys Asp Met Asn Ser Ala Asn Arg
 275 280 285
 Leu Ile Gln Gly Leu Phe Asp Gly Leu Asp Gly Gln Glu Ser Tyr Phe
 290 295 300
 Lys Lys Val Thr Gly Phe Ser Ser Tyr Tyr Asn Phe Ile Lys Gly Asp
 305 310 315 320
 Glu Glu Ser Lys Gln Asp Ser Val Leu Met Glu Phe Leu Ser Asn Pro
 325 330 335
 Glu Val Arg Lys Gly Ile His Val Gly Glu Leu Pro Phe His Asp Ser
 340 345 350
 Asp Gly His Asn Lys Val Ala Glu Met Leu Ser Glu Asp Thr Leu Asp
 355 360 365
 Thr Val Ala Pro Trp Val Ser Lys Leu Leu Ser His Tyr Arg Val Leu
 370 375 380
 Phe Tyr Asn Gly Gln Leu Asp Ile Ile Cys Ala Tyr Pro Met Thr Val
 385 390 395 400
 Asp Phe Leu Met Lys Met Pro Phe Asp Gly Asp Ser Glu Tyr Lys Arg
 405 410 415
 Ala Asn Arg Glu Ile Tyr Arg Val Asp Gly Glu Ile Ala Gly Tyr Lys
 420 425 430
 Lys Arg Ala Gly Arg Leu Gln Glu Val Leu Ile Arg Asn Ala Gly His
 435 440 445
 Met Val Pro Arg Asp Gln Pro Lys Trp Ala Phe Asp Met Ile Thr Ser
 450 455 460
 Phe Thr His Lys Asn Tyr Leu
 465 470

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 190283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile Arg Ala Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro Asp Gln
 20 25 30
 Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser Phe Arg
 35 40 45

Gln Tyr Ser Gly Tyr Leu Lys Ser Ser Gly Ser Lys His Leu His Tyr
 50 55 60
 Trp Phe Val Glu Ser Gln Lys Asp Pro Glu Asn Ser Pro Val Val Leu
 65 70 75 80
 Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Thr
 85 90 95
 Glu His Gly Pro Phe Leu Val Gln Pro Asp Gly Val Thr Leu Glu Tyr
 100 105 110
 Asn Pro Tyr Ser Trp Asn Leu Ile Ala Asn Val Leu Tyr Leu Glu Ser
 115 120 125
 Pro Ala Gly Val Gly Phe Ser Tyr Ser Asp Asp Lys Phe Tyr Ala Thr
 130 135 140
 Asn Asp Thr Glu Val Ala Gln Ser Asn Phe Glu Ala Leu Gln Asp Phe
 145 150 155 160
 Phe Arg Leu Phe Pro Glu Tyr Lys Asn Asn Lys Leu Phe Leu Thr Gly
 165 170 175
 Glu Ser Tyr Ala Gly Ile Tyr Ile Pro Thr Leu Ala Val Leu Val Met
 180 185 190
 Gln Asp Pro Ser Met Asn Leu Gln Gly Leu Ala Val Gly Asn Gly Leu
 195 200 205
 Ser Ser Tyr Glu Gln Asn Asp Asn Ser Leu Val Tyr Phe Ala Tyr Tyr
 210 215 220
 His Gly Leu Leu Gly Asn Arg Leu Trp Ser Ser Leu Gln Thr His Cys
 225 230 235 240
 Cys Ser Gln Asn Lys Cys Asn Phe Tyr Asp Asn Lys Asp Leu Glu Cys
 245 250 255
 Val Thr Asn Leu Gln Glu Val Ala Arg Ile Val Gly Asn Ser Gly Leu
 260 265 270
 Asn Ile Tyr Asn Leu Tyr Ala Pro Cys Ala Gly Gly Val Pro Ser His
 275 280 285
 Phe Arg Tyr Glu Lys Asp Thr Val Val Val Gln Asp Leu Gly Asn Ile
 290 295 300
 Phe Thr Arg Leu Pro Leu Lys Arg Met Trp His Gln Ala Leu Leu Arg
 305 310 315 320
 Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr Thr Ala
 325 330 335
 Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu Asn Ile
 340 345 350
 Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val Asn Leu
 355 360 365
 Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu Lys Leu
 370 375 380
 Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp Val Asp
 385 390 395 400
 Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser Leu Asn
 405 410 415
 Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr Gly Asp
 420 425 430
 Ser Gly Glu Gln Ile Ala Gly Phe Val Lys Glu Phe Ser His Ile Ala
 435 440 445
 Phe Leu Thr Ile Lys Gly Ala Gly His Met Val Pro Thr Asp Lys Pro
 450 455 460
 Leu Ala Ala Phe Thr Met Phe Ser Arg Phe Leu Asn Lys Gln Pro Tyr
 465 470 475 480